Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 00:35:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081173.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR3081173 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081173.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 00:35:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081173.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,524,115
Mapped reads	2,291,722 / 90.79%
Unmapped reads	232,393 / 9.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,305 / 0.8%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	84,690 / 3.36%
Duplication rate	2.56%
Clipped reads	1,031,658 / 40.87%

2.2. ACGT Content

Number/percentage of A's	44,147,162 / 28.71%
Number/percentage of C's	28,768,056 / 18.71%
Number/percentage of T's	47,386,884 / 30.82%
Number/percentage of G's	33,400,203 / 21.72%
Number/percentage of N's	44,903 / 0.03%
GC Percentage	40.44%

2.3. Coverage

Mean	0.0497

Standard Deviation	0.4802

2.4. Mapping Quality

Mean Mapping Quality	45.85

2.5. Mismatches and indels

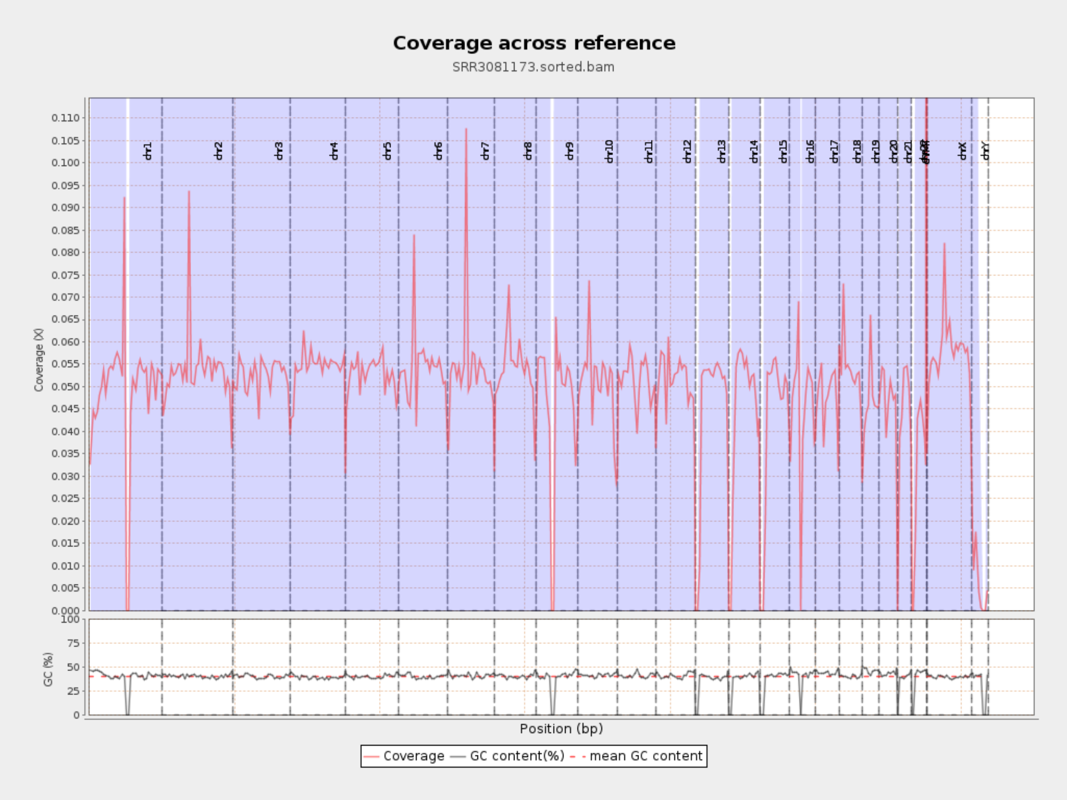
General error rate	0.89%
Mismatches	1,347,154
Insertions	12,819
Mapped reads with at least one insertion	0.55%
Deletions	40,442
Mapped reads with at least one deletion	1.75%
Homopolymer indels	45.2%

2.6. Chromosome stats

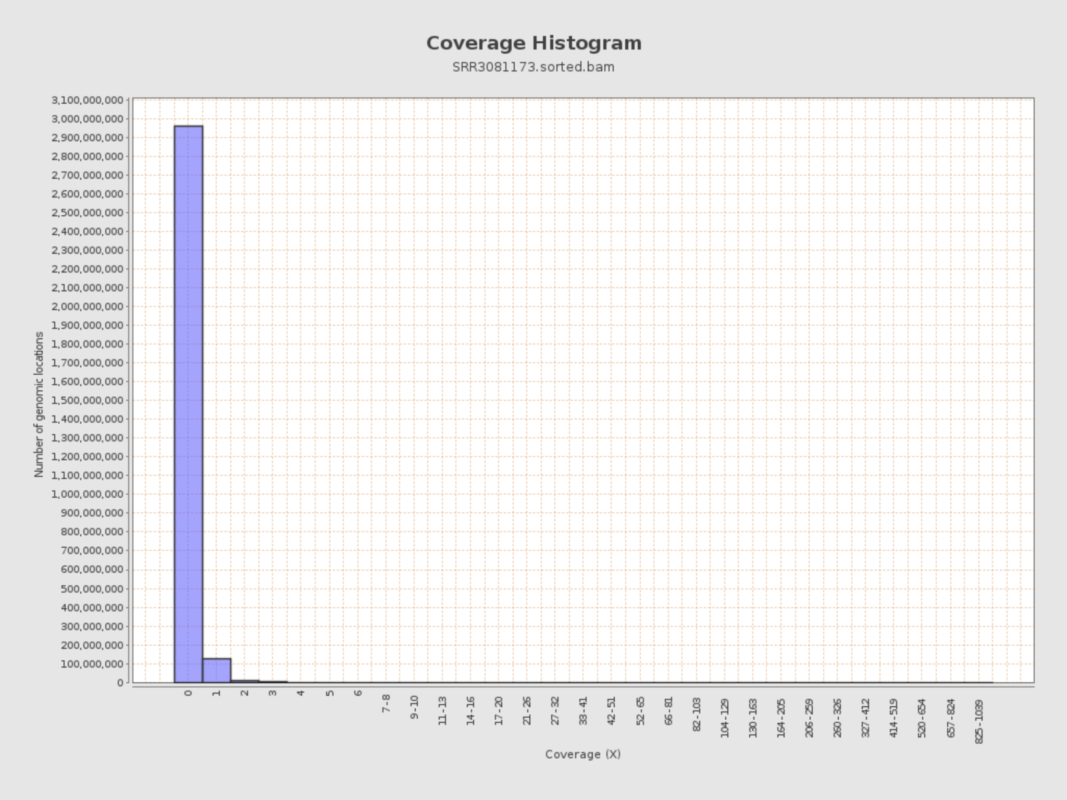
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12207943	0.049	0.9226
chr2	243199373	13113752	0.0539	0.5208
chr3	198022430	10419881	0.0526	0.2503
chr4	191154276	10420115	0.0545	0.2687
chr5	180915260	9571551	0.0529	0.255
chr6	171115067	9286618	0.0543	0.3866
chr7	159138663	8752841	0.055	0.7814

chr8	146364022	7899317	0.054	0.6013
chr9	141213431	6496988	0.046	0.4225
chr10	135534747	6932095	0.0511	0.3748
chr11	135006516	6918060	0.0512	0.427
chr12	133851895	6911084	0.0516	0.2562
chr13	115169878	5049560	0.0438	0.2288
chr14	107349540	4723669	0.044	0.2686
chr15	102531392	4285743	0.0418	0.2333
chr16	90354753	4079389	0.0451	0.2797
chr17	81195210	3823953	0.0471	0.2976
chr18	78077248	4257869	0.0545	0.8989
chr19	59128983	2771459	0.0469	0.6125
chr20	63025520	2991754	0.0475	0.2538
chr21	48129895	2041600	0.0424	0.2477
chr22	51304566	1516672	0.0296	0.1852
chrMT	16571	10898	0.6577	0.9298
chrX	155270560	8966041	0.0577	0.3164
chrY	59373566	364176	0.0061	0.1251

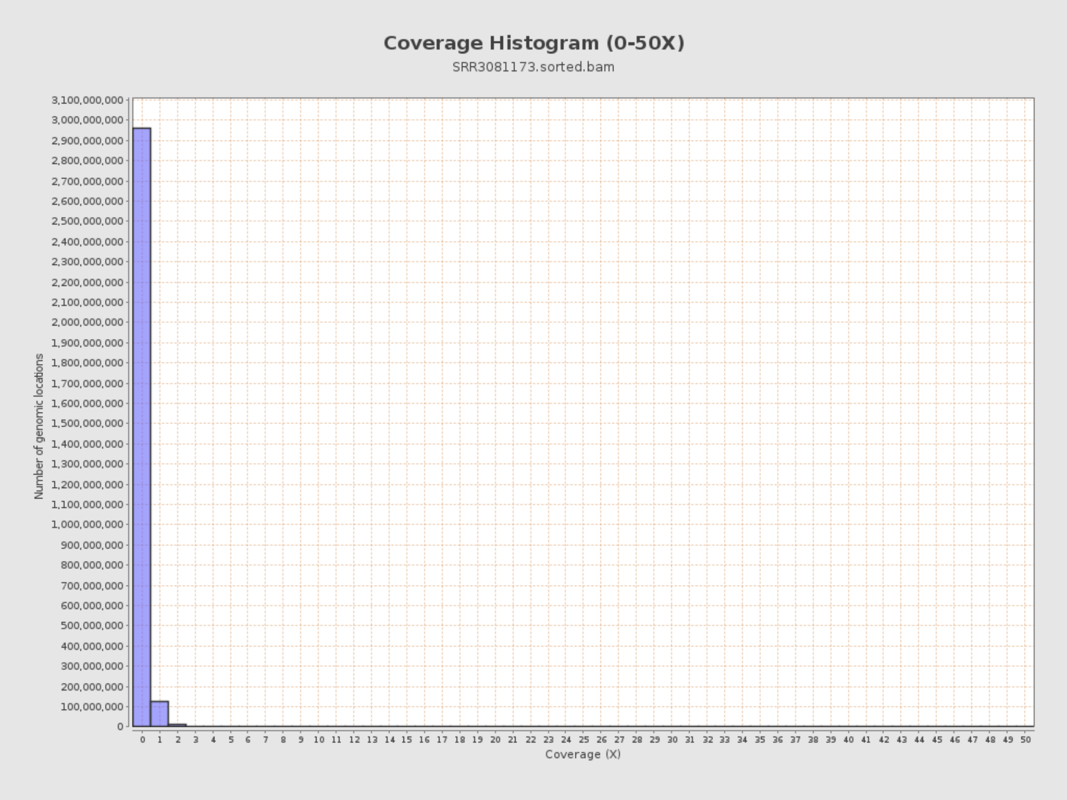
3. Results : Coverage across reference



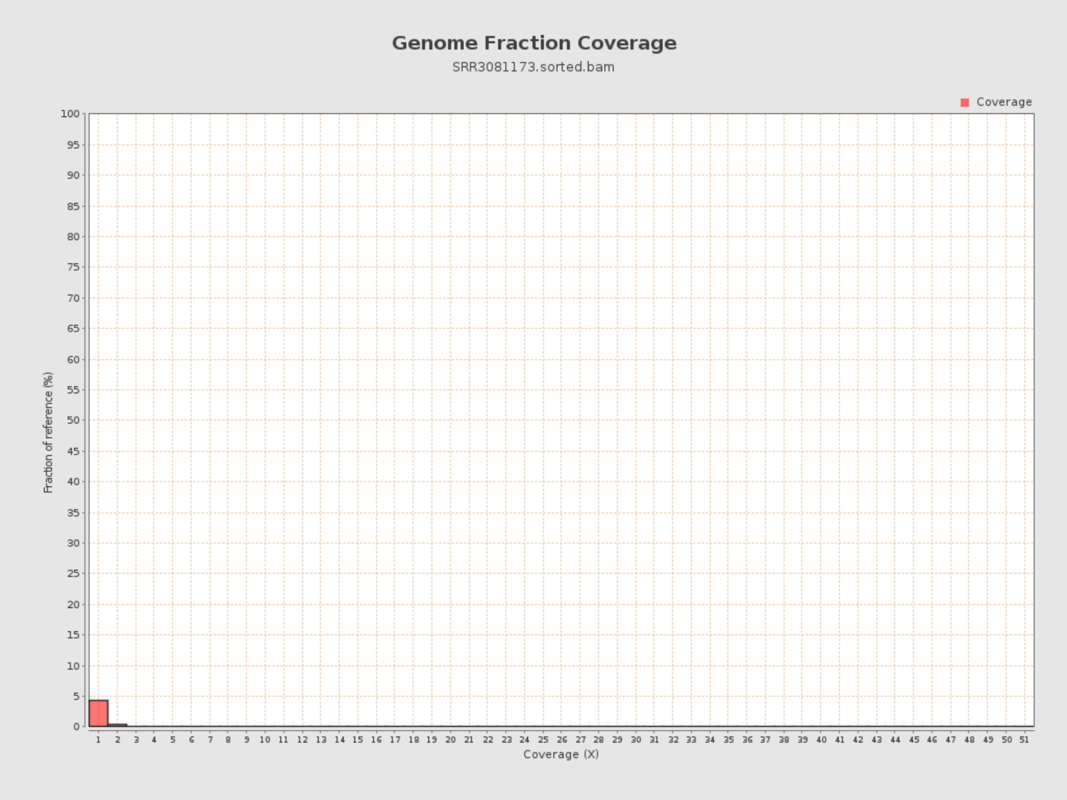
4. Results : Coverage Histogram



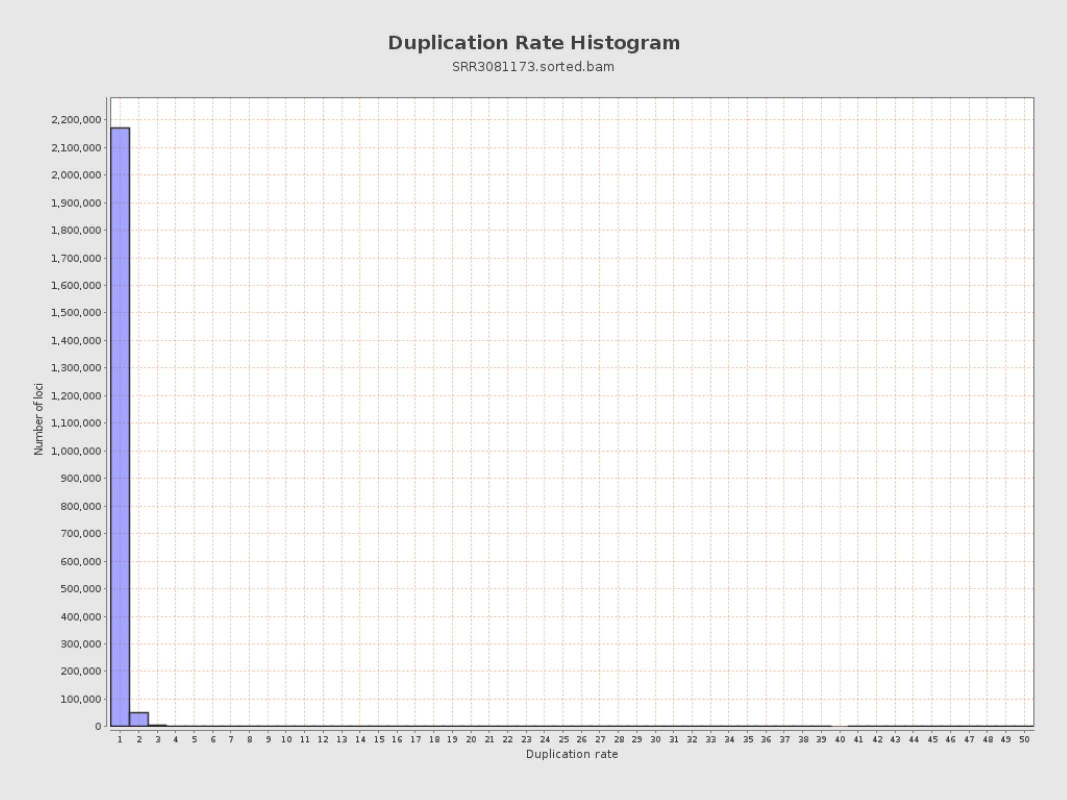
5. Results : Coverage Histogram (0-50X)



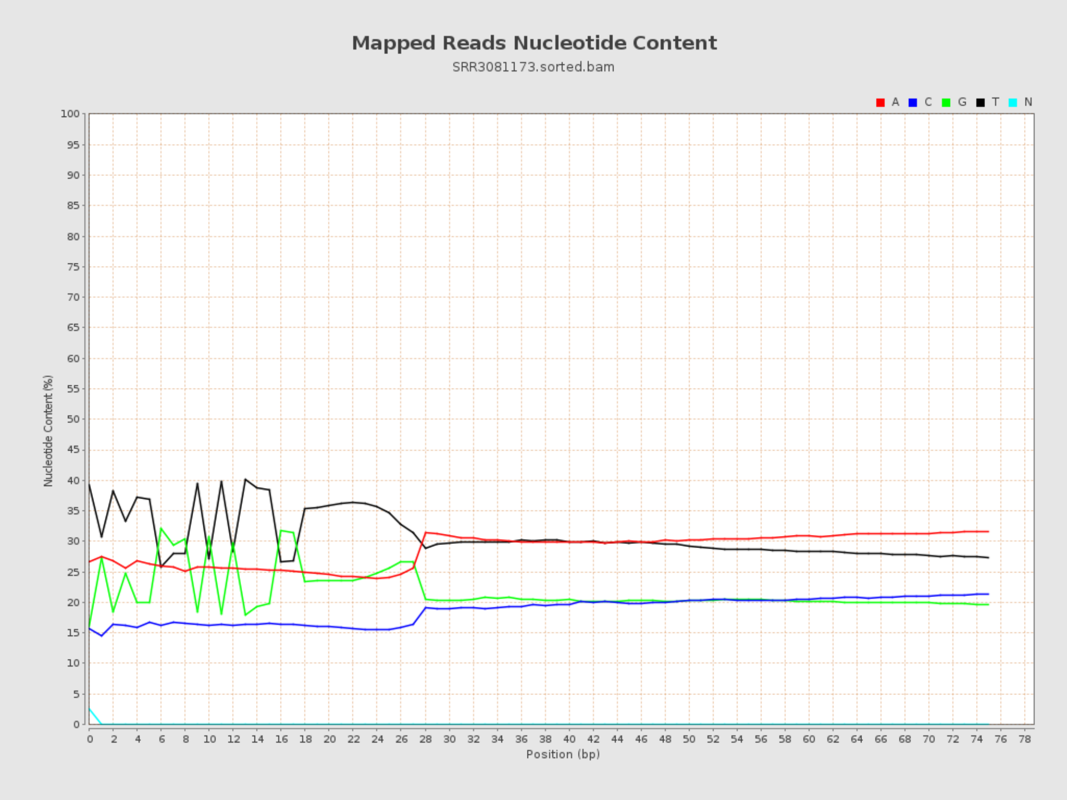
6. Results : Genome Fraction Coverage



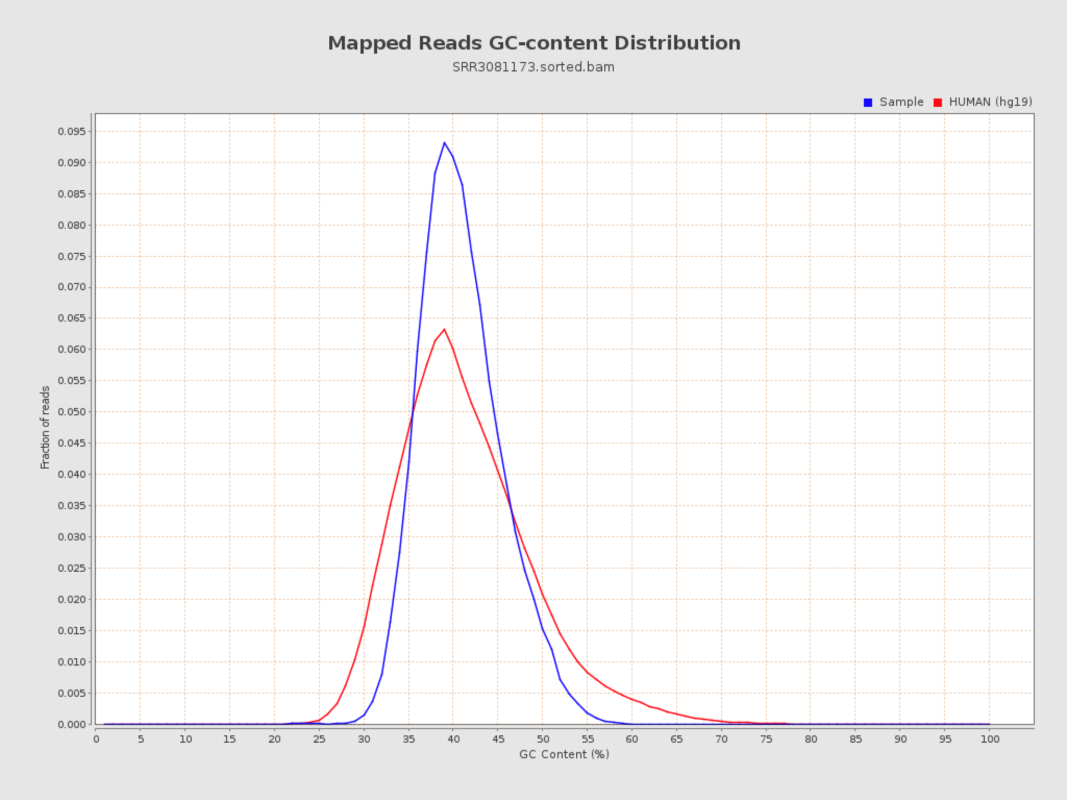
7. Results : Duplication Rate Histogram



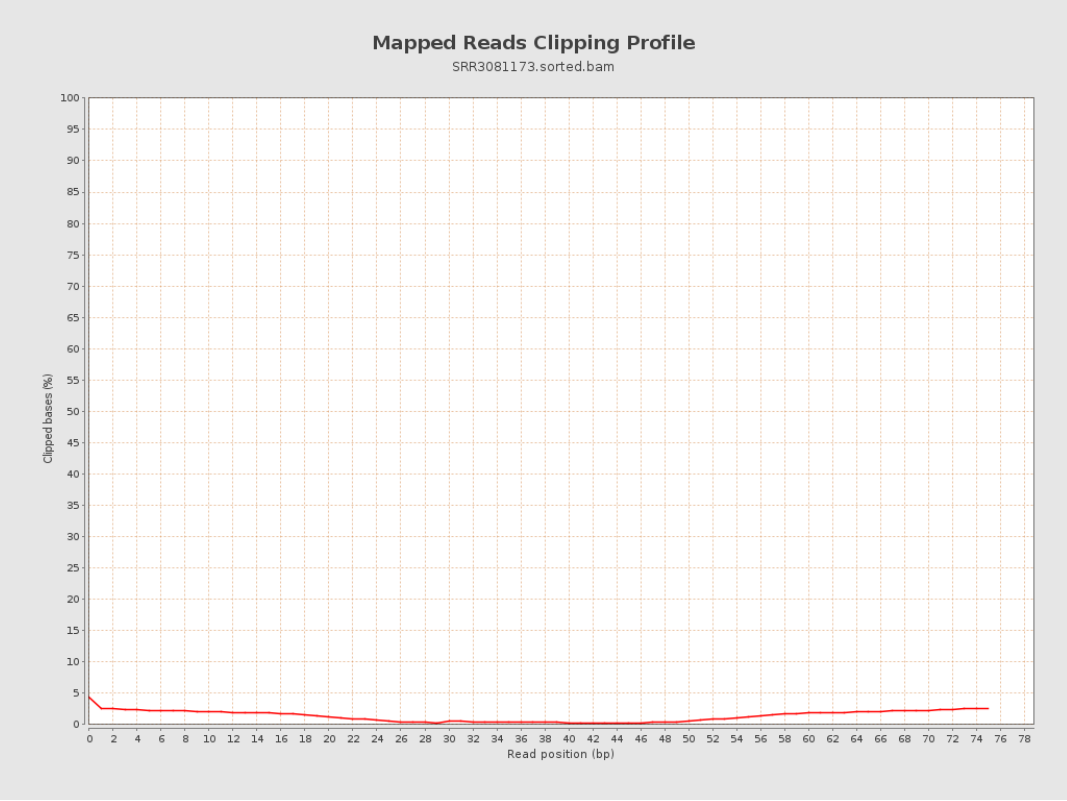
8. Results : Mapped Reads Nucleotide Content



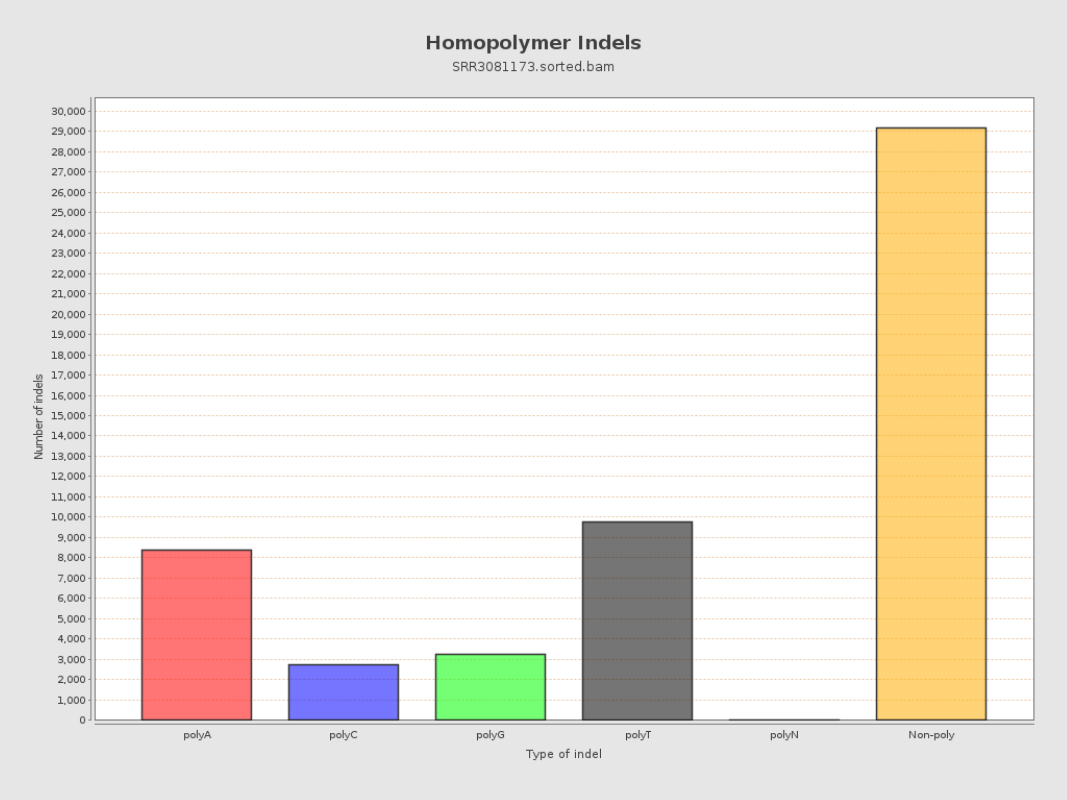
9. Results : Mapped Reads GC-content Distribution



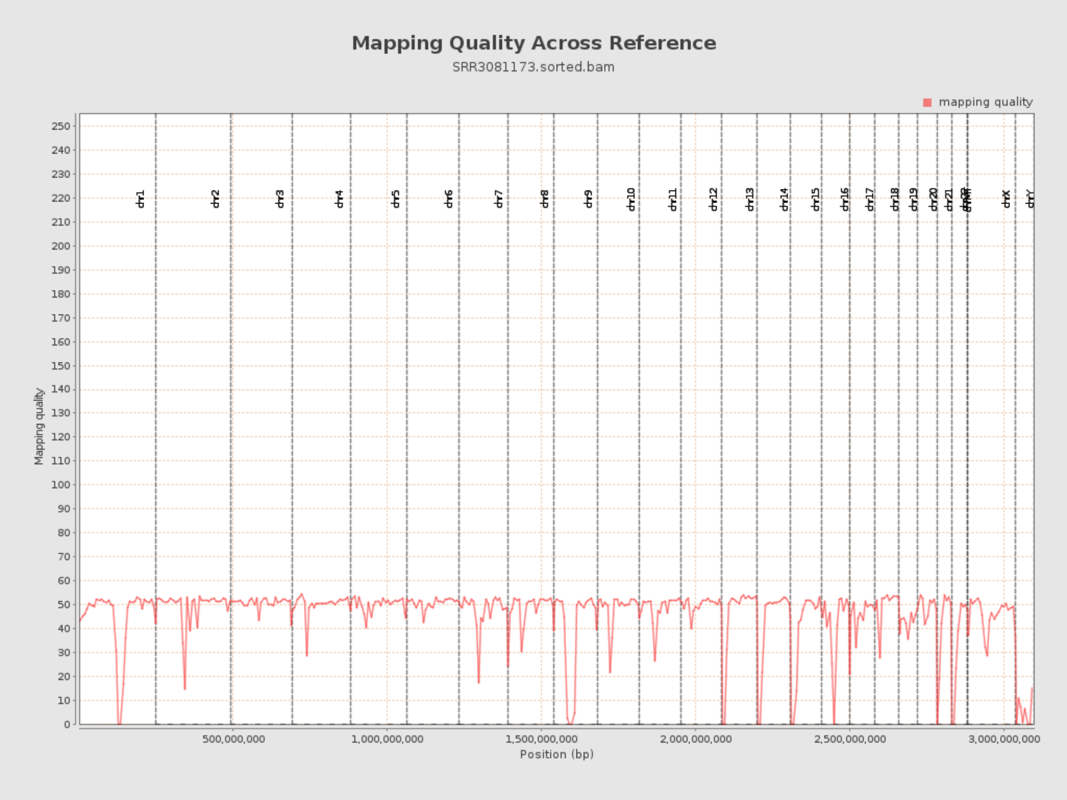
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram